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Search	Most Recent Queries	Time	Result
#27	Search #26 AND (CTL or T-cell or "t cell") Field: Title/Abstract , Limits: Publication Date to 1995	17:31:18	16
#26	Search (malaria OR plasmodium OR falciparum) AND ("liver stage" OR liver-stage OR LSA*) Field: Title/Abstract , Limits: Publication Date to 1995	17:30:42	64
#19	Related Articles for PubMed (Select 2143519)	16:56:16	136
#14	Search (B-cell or "B cell" or antibod*) AND epitope AND (malaria OR plasmodium OR falciparum) AND ("liver stage" OR liver-stage OR LSA*)	16:54:05	24
#9	Search epitope AND repeat AND (plasmodium OR falciparum) AND ("liver stage" OR liver-stage OR LSA*)	16:53:35	9
#13	Related Articles for PubMed (Select 12135271)	11:01:26	602
#8	Search eptiope AND repeat AND (plasmodium or falciparum) AND ("liver stage" or liver-stage or LSA*)	09:53:02	0
#6	Search (marchand[au] or guerlin-marchand[au]) AND epitope AND (plasmodium or falciparum)	09:28:13	3

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		<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L8	L6 and (@ad<19910205 or @pd<19920205)	1
<input type="checkbox"/>	L7	l5 and l6	28
<input type="checkbox"/>	L6	(t adj (cell or lymphocyte) or cellular) with Epitope and (LSA\$2 or (liver-stage or liver adj stage) adj3 (protein or antigen)) with (malaria or plasmodium or falciparum)	124
<input type="checkbox"/>	L5	(malaria or plasmodium or falciparum) same(immunoassay or (detect\$ or determin\$) with (antibod\$6 or immunoglob\$9))	543
<input type="checkbox"/>	L4	L1 and (@ad<19910205 or @pd<19920205)	85
<input type="checkbox"/>	L3	L1 and fusion same (epitop\$3 or peptides)	206
<input type="checkbox"/>	L2	(malaria or plasmodium or falciparum) same(immunoassay or (detect\$ or determin\$) with (antibod\$6 or immunoglob\$9))	543
<input type="checkbox"/>	L1	(malaria or plasmodium or falciparum) same(immunoassay or (detect\$ or determin\$) with (antibod\$6 or immunoglob\$9))	543

END OF SEARCH HISTORY

BLASTN 2.2.14 [May-07-2006]

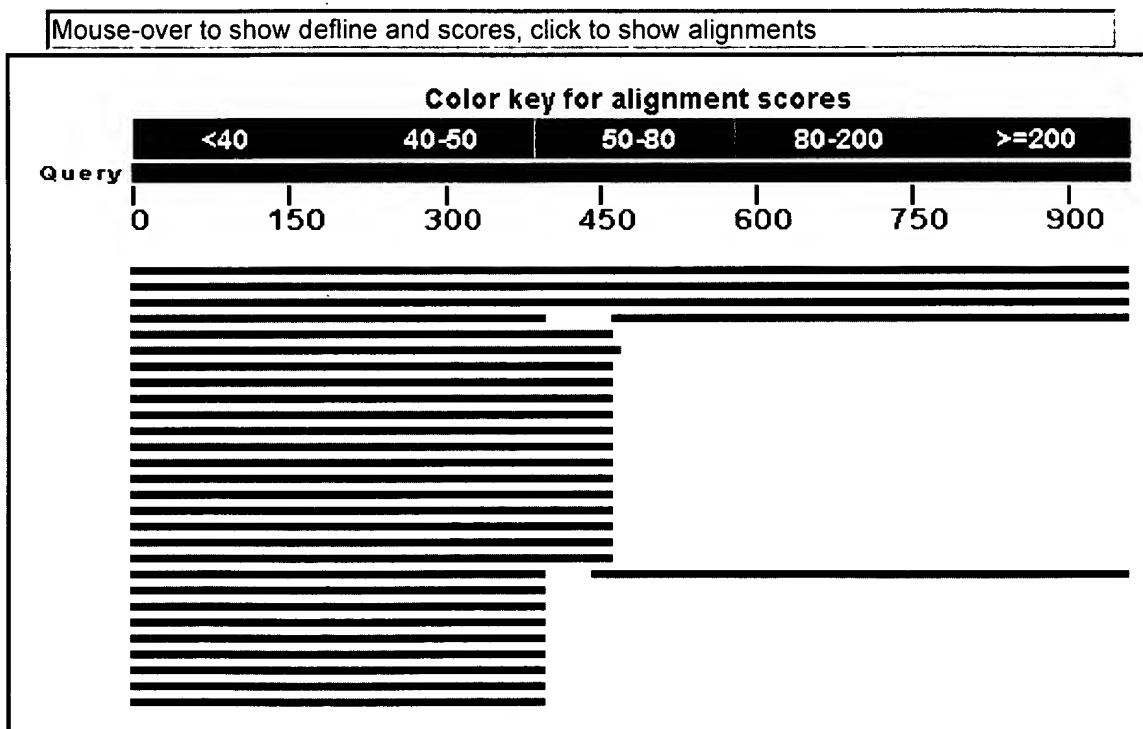
RID: 1158783042-7538-80683885490.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
4,365,567 sequences; 18,294,867,195 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
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Query= *SEQ 10 NO: 38*
Length=954

Distribution of 184 Blast Hits on the Query Sequence



[Distance tree of results](#) NEW

Sequences producing significant alignments:		Score (Bits)	E Value
gi 510185 emb Z30319.1 PFLSA15	P.falciparum LSA-1 gene for liver	1729	0.0
gi 9915 emb X56203.1 PFLSA1G	P.falciparum LSA-1 gene for liver s	1635	0.0
gi 23495173 gb AE014834.1 	Plasmodium falciparum 3D7 chromoso...	1526	0.0
gi 510183 emb Z30320.1 PFLSA13	P.falciparum LSA-1 gene for liver	821	0.0
gi 950655 gb L40911.1 PFALSA1D	Plasmodium falciparum (clones ...	815	0.0
gi 1435204 gb U60974.1 PFU60974	Plasmodium falciparum liver s...	811	0.0
gi 725321 gb L40942.1 PFALSA1P	Plasmodium falciparum (clone K...	809	0.0
gi 725319 gb L40941.1 PFALSA1O	Plasmodium falciparum (clones ...	809	0.0

gi 725311 gb L40946.1 PFALSA1K	Plasmodium falciparum (clone B...	809	0.0
gi 950658 gb L40914.1 PFALSA1H	Plasmodium falciparum (clone K...	809	0.0
gi 950656 gb L40912.1 PFALSA1E	Plasmodium falciparum (clone K...	809	0.0
gi 725325 gb L40944.1 PFALSA1R	Plasmodium falciparum (clones ...	804	0.0
gi 725323 gb L40943.1 PFALSA1Q	Plasmodium falciparum (clones ...	804	0.0
gi 950657 gb L40913.1 PFALSA1F	Plasmodium falciparum (clone K...	804	0.0
gi 950661 gb L40922.1 PFALSA1L	Plasmodium falciparum (clone K...	798	0.0
gi 950660 gb L40918.1 PFALSA1J	Plasmodium falciparum (clone K...	798	0.0
gi 950659 gb L40917.1 PFALSA1I	Plasmodium falciparum (clone K...	787	0.0
gi 950662 gb L40923.1 PFALSA1M	Plasmodium falciparum (clone K...	782	0.0
gi 725291 gb L40945.1 PFALSA1	Plasmodium falciparum (clone BR...	776	0.0
gi 3643906 gb AF086796.1 AF086796	Plasmodium falciparum strai...	723	0.0
gi 3643900 gb AF086793.1 AF086793	Plasmodium falciparum strai...	723	0.0
gi 3643918 gb AF086802.1 AF086802	Plasmodium falciparum strai...	712	0.0
gi 3643912 gb AF086799.1 AF086799	Plasmodium falciparum strai...	712	0.0
gi 3643910 gb AF086798.1 AF086798	Plasmodium falciparum strai...	712	0.0
gi 3643916 gb AF086801.1 AF086801	Plasmodium falciparum strai...	706	0.0
gi 3643914 gb AF086800.1 AF086800	Plasmodium falciparum strai...	706	0.0
gi 3643908 gb AF086797.1 AF086797	Plasmodium falciparum strai...	706	0.0
gi 3643904 gb AF086795.1 AF086795	Plasmodium falciparum strai...	706	0.0
gi 3643902 gb AF086794.1 AF086794	Plasmodium falciparum strai...	706	0.0
gi 160367 gb M28266.1 PFALIVANT	Plasmodium falciparum liver-stag	287	5e-74

Alignments

Get selected sequences	Select all	Deselect all	Distance tree of results
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> [gi|510185|emb|Z30319.1|PFLSA15](#) P.falciparum LSA-1 gene for liver stage antigen-1 (5')
Length=988

Score = 1729 bits (936), Expect = 0.0
Identities = 954/954 (100%), Gaps = 0/954 (0%)
Strand=Plus/Plus

Query	1	ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTGATATTTTCAT	60
Sbjct	33	92
Query	61	ATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCATAAAATCTAACTTGAGA	120
Sbjct	93	152
Query	121	AGTGGTTCTTCAAATTCTAGGAATCGAATAAATGAGGAAAATCACGAGAAGAAACACGTT	180
Sbjct	153	212
Query	181	TTATCTCATAATTCATATGAGAAAATAAAATAATGAAAATAATAAATTTTTCGATAAG	240
Sbjct	213	272
Query	241	GATAAAGAGTTAACGATGTCTAATGTAAAAAATGTGTACAAACAAATTTCAAAGTCTT	300
Sbjct	273	332
Query	301	TTAAGAAATCTTGGTGTTTCAGAGAATATATTCCTTAAAGAAAATAAATTAAATAAGGAA	360
Sbjct	333	392
Query	361	GGGAAATTAATTGAACACATAATAAATGATGATGACGATaaaaaaaaTATATTAAAGGG	420
Sbjct	393	452
Query	421	CAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAGCAGCTAAAGAAAAGTTACAGGGG	480
Sbjct	453	512
Query	481	CAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGC	540
Sbjct	513	572
Query	541	GATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAA	600
Sbjct	573	632

Query	601	CAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGA	660
Sbjct	633	692
Query	661	CTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAA	720
Sbjct	693	752
Query	721	GAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTG	780
Sbjct	753	812
Query	781	CAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTACAAGAGCAG	840
Sbjct	813	872
Query	841	CAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGAT	900
Sbjct	873	932
Query	901	TTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGAACAACAAAGCGATTTA	954
Sbjct	933	986

Score = 713 bits (386), Expect = 0.0
Identities = 426/446 (95%), Gaps = 0/446 (0%)
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	543G..A.AA.....T.....T.....	602
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	603G.....	662
Query	580	GAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	663T.....	722
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	699
Sbjct	723G.....	782
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG	759
Sbjct	783	842
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	843T.....A.....G..G.....T.....	902
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	903G.....A..A.....G....G.....G.	962
Query	880	TTGCAAGAACAACAAAGCGATTTAGA	905
Sbjct	963	988

> [gi|9915|emb|X56203.1|PFLSA1G](#) P.falciparum LSA-1 gene for liver stage antigen
Length=5970

Score = 1635 bits (885), Expect = 0.0
Identities = 937/954 (98%), Gaps = 0/954 (0%)
Strand=Plus/Plus

Query	1	ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTGATATTTTCAT	60
Sbjct	79	138
Query	61	ATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCATAAATCTAACTTGAGA	120
Sbjct	139	198
Query	121	AGTGGTTCTTCAAATTCTAGGAATCGAATAAATGAGGAAAATCACGAGAAGAAACACGTT	180
Sbjct	199G.....	258

Query	181	TTATCTCATAATTCATATGAGAAACTAAAAATAATGAAAATAATAAATTTTTTCGATAAG	240
Sbjct	259	318
Query	241	GATAAAGAGTTAACGATGTCTAATGTAAAAAATGTGTACAAACAAATTTCAAAGTCTT	300
Sbjct	319	378
Query	301	TTAAGAAATCTTGGTGTTCAGAGAATATATTCCTTAAAGAAAATAAATTAATAAGGAA	360
Sbjct	379	438
Query	361	GGGAAATTAATTGAACACATAATAAATGATGATGACGATaaaaaaaaTATATTAAAGGG	420
Sbjct	439	498
Query	421	CAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAGCAGCTAAAGAAAAGTTACAGGGG	480
Sbjct	499C.....	558
Query	481	CAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGC	540
Sbjct	559T.....T.....	618
Query	541	GATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAA	600
Sbjct	619C.....	678
Query	601	CAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGA	660
Sbjct	679T.....A.....G..G.....	738
Query	661	CTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAA	720
Sbjct	739G..G.....	798
Query	721	GAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTG	780
Sbjct	799	858
Query	781	CAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTACAAGAGCAG	840
Sbjct	859G.....G.....A..A	918
Query	841	CAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGAT	900
Sbjct	919G.....	978
Query	901	TTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	954
Sbjct	979A.....	1032

Score = 848 bits (459), Expect = 0.0
Identities = 483/495 (97%), Gaps = 0/495 (0%)
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	2476A.A.....T.....	2535
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	2536	2595
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	2596	2655
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	699
Sbjct	2656T.....A.....G.....	2715
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG	759
Sbjct	2716	2775
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	2776	2835
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	2836G.....A.....A.....G....G.....	2895

Query	880	TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGAA	939
Sbjct	2896A.....	2955

Query	940	CAACAAAGCGATTTA	954
Sbjct	2956	2970

Score = 843 bits (456), Expect = 0.0
 Identities = 482/495 (97%), Gaps = 0/495 (0%)
 Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	1201G..A.AA.....T.....T....T.....	1260
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	1261A.....G.....	1320
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	1321	1380
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	699
Sbjct	1381	1440
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG	759
Sbjct	1441	1500
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	1501	1560
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	1561G.....	1620
Query	880	TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGGTTGCAAGAA	939
Sbjct	1621C.....T.....A.....	1680
Query	940	CAACAAAGCGATTTA	954
Sbjct	1681	1695

Score = 832 bits (450), Expect = 0.0
 Identities = 480/495 (96%), Gaps = 0/495 (0%)
 Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	3904G..A.AA.....T.....	3963
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	3964	4023
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	4024T.....	4083
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	699
Sbjct	4084G.....	4143
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG	759
Sbjct	4144T.....A.....	4203
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	4204T.....	4263
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	4264A.....A.....G....G.....	4323
Query	880	TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGGTTGCAAGAA	939

Sbjct . 4324 A 4383

Query 940 CAACAAAGCGATTTA 954
Sbjct 4384 4398

Score = 832 bits (450), Expect = 0.0
Identities = 480/495 (96%), Gaps = 0/495 (0%)
Strand=Plus/Plus

Query 460 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA 519
Sbjct 4159 A . AA T 4218

Query 520 AAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA 579
Sbjct 4219 T A 4278

Query 580 GAACAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA 639
Sbjct 4279 .. G A 4338

Query 640 AGCGATTTCAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTC 699
Sbjct 4339 G 4398

Query 700 GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAG 759
Sbjct 4399 4458

Query 760 AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACTTGCT 819
Sbjct 4459 4518

Query 820 AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTCAGAACAAGATAGACTTGCTAAAGAAAAG 879
Sbjct 4519 G A A G G 4578

Query 880 TTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAA 939
Sbjct 4579 A 4638

Query 940 CAACAAAGCGATTTA 954
Sbjct 4639 4653

Score = 832 bits (450), Expect = 0.0
Identities = 480/495 (96%), Gaps = 0/495 (0%)
Strand=Plus/Plus

Query 460 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA 519
Sbjct 4312 G . A . AA T 4371

Query 520 AAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA 579
Sbjct 4372 G 4431

Query 580 GAACAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA 639
Sbjct 4432 4491

Query 640 AGCGATTTCAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTC 699
Sbjct 4492 G A 4551

Query 700 GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAG 759
Sbjct 4552 4611

Query 760 AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACTTGCT 819
Sbjct 4612 4671

Query 820 AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTCAGAACAAGATAGACTTGCTAAAGAAAAG 879
Sbjct 4672 .. T G A A G G 4731

Query 880 TTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAA 939
Sbjct 4732 A 4791

Query 940 CAACAAAGCGATTTA 954
Sbjct 4792 4806

Score = 822 bits (445), Expect = 0.0
Identities = 479/496 (96%), Gaps = 0/496 (0%)
Strand=Plus/Plus

Query 459 AGCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGA 518
Sbjct 3801G.....A.A.....T..... 3860

Query 519 AAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCA 578
Sbjct 3861C...G..... 3920

Query 579 AGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACA 638
Sbjct 3921 3980

Query 639 AAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTT 698
Sbjct 3981 4040

Query 699 AGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGA 758
Sbjct 4041T..... 4100

Query 759 GAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGC 818
Sbjct 4101 4160

Query 819 TAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAA 878
Sbjct 4161A..A.....G...G..... 4220

Query 879 GTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGA 938
Sbjct 4221T....T.....A...A..... 4280

Query 939 ACAACAAAGCGATTTA 954
Sbjct 4281 G.....A..... 4296

Score = 821 bits (444), Expect = 0.0
Identities = 476/492 (96%), Gaps = 0/492 (0%)
Strand=Plus/Plus

Query 460 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAA 519
Sbjct 1354G..A.AA.....T.....T..... 1413

Query 520 AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA 579
Sbjct 1414G..... 1473

Query 580 GAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA 639
Sbjct 1474 1533

Query 640 AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA 699
Sbjct 1534A.....G..G..... 1593

Query 700 GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG 759
Sbjct 1594T.....C..... 1653

Query 760 AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT 819
Sbjct 1654T..... 1713

Query 820 AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG 879
Sbjct 1714G..... 1773

Query 880 TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGAA 939
Sbjct 1774T.....A..... 1833

Query 940 CAACAAAGCGAT 951
Sbjct 1834 1845

Score = 815 bits (441), Expect = 0.0
Identities = 477/495 (96%), Gaps = 0/495 (0%)
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	3853G..A.AA.....T.....C.....	3912
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	3913G.....	3972
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	3973T.....	4032
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTA	699
Sbjct	4033	4092
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAG	759
Sbjct	4093	4152
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	4153T.....A.....G....	4212
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	4213G.....A..A.....	4272
Query	880	TTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAA	939
Sbjct	4273	..A.....G.....A.....A.....	4332
Query	940	CAACAAAGCGATTTA 954	
Sbjct	4333 4347	

Score = 815 bits (441), Expect = 0.0
Identities = 477/495 (96%), Gaps = 0/495 (0%)
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	4261A.A.....A....T.....	4320
Query	520	AAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	4321G.....	4380
Query	580	GAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	4381	4440
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTA	699
Sbjct	4441G.....	4500
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAG	759
Sbjct	4501T.....G.....A.....	4560
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	4561G....	4620
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	4621G.....A..A.....G.....T.....	4680
Query	880	TTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAA	939
Sbjct	4681G.....A.....A.....	4740
Query	940	CAACAAAGCGATTTA 954	

Sbjct 4741 4755

Score = 809 bits (438), Expect = 0.0
Identities = 476/495 (96%), Gaps = 0/495 (0%)
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	2119G..A.AA.....T.....	2178
Query	520	AAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	2179G.....	2238
Query	580	GAACAACAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	2239	..G.....C.....	2298
Query	640	AGCGATTTCAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTC	699
Sbjct	2299G.....	2358
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAG	759
Sbjct	2359T....T.....A.....G.....	2418
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACTTGCT	819
Sbjct	2419T.....	2478
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTCAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	2479A.....G....G.....	2538
Query	880	TTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAA	939
Sbjct	2539T.....A.....	2598
Query	940	CAACAAAGCGATTTC	954
Sbjct	2599	2613

Score = 809 bits (438), Expect = 0.0
Identities = 476/495 (96%), Gaps = 0/495 (0%)
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	2272G..A.AA.....T.....	2331
Query	520	AAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	2332T.....A...	2391
Query	580	GAACAACAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	2392	..G.....	2451
Query	640	AGCGATTTCAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTC	699
Sbjct	2452T.....A.....G.....	2511
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAG	759
Sbjct	2512	2571
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACTTGCT	819
Sbjct	2572T.....G....	2631
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTCAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	2632G.....A..A.....	2691
Query	880	TTGCAAGAACAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAA	939
Sbjct	2692	..A.....G.....A.....	2751
Query	940	CAACAAAGCGATTTC	954
Sbjct	2752	2766

Score = 809 bits (438), Expect = 0.0
Identities = 476/495 (96%), Gaps = 0/495 (0%)
Strand=Plus/Plus

Query	460	GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTTCAGAACAAGAGAGACGTGCTAAAGAA	519
Sbjct	3955G..A.AA.....T.....T.....	4014
Query	520	AAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAA	579
Sbjct	4015	4074
Query	580	GAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAA	639
Sbjct	4075	4134
Query	640	AGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTA	699
Sbjct	4135A.....	4194
Query	700	GAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAG	759
Sbjct	4195T	4254
Query	760	AGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCT	819
Sbjct	4255T.....A.....G.....A.....G....	4314
Query	820	AAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAG	879
Sbjct	4315G.....A..A.....G....G.....	4374
Query	880	TTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAGGTTGCAAGAA	939
Sbjct	4375A.....	4434
Query	940	CAACAAAGCGATTTA	954
Sbjct	4435	4449

Score = 808 bits (437), Expect = 0.0
Identities = 490/515 (95%), Gaps = 5/515 (0%)
Strand=Plus/Plus

Query	442	GATCTTGAAGAA-AAAG-C-AGCTAAAGAAAAGTTACAGGGGCAACAAAGCGAT-TCAGA	497
Sbjct	1129A...C..G.G..A.T.....C.-...	1187
Query	498	ACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAG	557
Sbjct	1188T.....T..	1247
Query	558	ACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAA	617
Sbjct	1248A.....G.....T.....	1307
Query	618	AGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTT	677
Sbjct	1308G.....	1367
Query	678	GCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACA	737
Sbjct	1368T.....	1427
Query	738	ACAAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGA	797
Sbjct	1428	1487
Query	798	TTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACA	857
Sbjct	1488G.....G.....A..A.....	1547
Query	858	AGATAGACTTGCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACG	917
Sbjct	1548	...G.....A.....G..G.....T	1607
Query	918	TGCTAAAGAAAGGTTGCAAGAACAACAAAGCGATT	952
Sbjct	1608A.....	1642

BLASTX 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1158786675-8897-80331541551.BLASTQ4

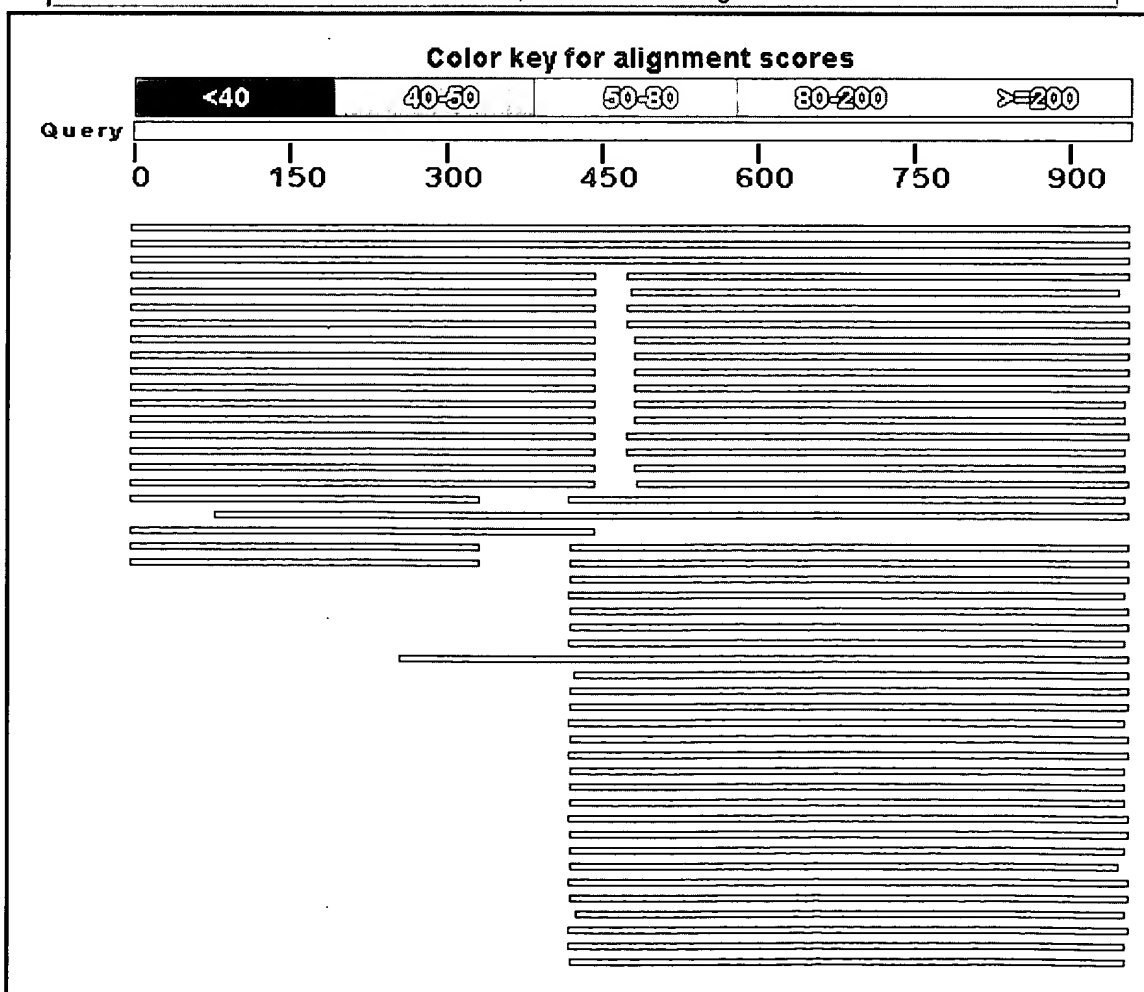
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
4,002,069 sequences; 1,381,387,148 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query= *SEQ ID NO: 38 vs protein database*
Length=954

Distribution of 1417 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments





Sequences producing significant alignments:

	Score (Bits)	E Value	
gi 510186 emb CAA82974.1 liver stage antigen-1 [Plasmodium falc	441	2e-122	
gi 9916 emb CAA39663.1 liver stage antigen [Plasmodium falcipar	426	6e-118	
gi 23508159 ref NP_700829.1 liver stage antigen, putative [P...	402	9e-111	G
gi 510184 emb CAA82975.1 liver stage antigen-1 [Plasmodium falc	284	4e-75	
gi 725322 gb AAC41594.1 liver stage-specific antigen 1	149	2e-34	
gi 725300 gb AAC41583.1 liver stage-specific antigen 1	149	2e-34	
gi 725320 gb AAC41593.1 liver stage-specific antigen 1	147	5e-34	
gi 725302 gb AAC41584.1 liver stage-specific antigen 1	147	5e-34	
gi 725306 gb AAC41586.1 liver stage-specific antigen 1	147	7e-34	
gi 725310 gb AAC41588.1 liver stage-specific antigen 1	147	7e-34	
gi 725304 gb AAC41585.1 liver stage-specific antigen 1	147	7e-34	
gi 725312 gb AAC41589.1 liver stage-specific antigen 1	147	9e-34	
gi 1435205 gb AAB04062.1 liver stage antigen-1	146	1e-33	
gi 725326 gb AAC41596.1 liver stage-specific antigen 1	145	2e-33	
gi 725324 gb AAC41595.1 liver stage-specific antigen 1	145	3e-33	
gi 725308 gb AAC41587.1 liver stage-specific antigen 1	144	8e-33	
gi 725314 gb AAC41590.1 liver stage-specific antigen 1	142	2e-32	
gi 725316 gb AAC41591.1 liver stage-specific antigen 1	142	2e-32	
gi 3643901 gb AAC42977.1 liver stage-specific antigen-1 [Pla...	140	7e-32	
gi 58429870 gb AAW78331.1 LSA-NRC [synthetic construct]	140	1e-31	
gi 725292 gb AAC41581.1 liver stage-specific antigen 1	140	1e-31	
gi 3643903 gb AAC42978.1 liver stage-specific antigen-1 [Pla...	139	2e-31	
gi 3643919 gb AAC42986.1 liver stage-specific antigen-1 [Plasmo	137	6e-31	
gi 82705890 ref XP_727156.1 hypothetical protein PY06496 [Pl...	122	3e-26	G
gi 225719 prf 1311343A antigen,liver stage specific	117	1e-24	
gi 109509645 ref XP_001066623.1 PREDICTED: hypothetical protein	115	4e-24	G
gi 109465334 ref XP_001075528.1 PREDICTED: hypothetical protein	112	3e-23	G
gi 66803152 ref XP_635419.1 hypothetical protein DDBDRAFT_01...	111	4e-23	G
gi 109467281 ref XP_001065891.1 PREDICTED: hypothetical protein	110	1e-22	G
gi 84998962 ref XP_954202.1 hypothetical protein TA20215 [Th...	109	2e-22	G
gi 109476246 ref XP_001061184.1 PREDICTED: hypothetical protein	108	3e-22	G
gi 109510232 ref XP_001063700.1 PREDICTED: similar to Cell d...	108	5e-22	G
gi 109509437 ref XP_001077753.1 PREDICTED: hypothetical protein	108	5e-22	G
gi 109472296 ref XP_001060556.1 PREDICTED: hypothetical protein	108	5e-22	G
gi 58429871 gb AAW78332.1 truncated LSA-NRC [synthetic construc	105	2e-21	
gi 66800837 ref XP_629344.1 SNF2-related domain-containing p...	105	2e-21	G
gi 109503258 ref XP_001072188.1 PREDICTED: hypothetical protein	105	4e-21	G
gi 68356608 ref XP_696335.1 PREDICTED: similar to Apoptotic ...	105	4e-21	G
gi 67479985 ref XP_655365.1 villidin [Entamoeba histolytica ...	105	4e-21	G
gi 109509610 ref XP_001063252.1 PREDICTED: hypothetical protein	104	5e-21	G
gi 109506221 ref XP_001073883.1 PREDICTED: hypothetical protein	104	5e-21	G
gi 109480113 ref XP_001063529.1 PREDICTED: hypothetical protein	103	9e-21	G
gi 68356430 ref XP_687786.1 PREDICTED: similar to Apoptotic ...	103	2e-20	G
gi 109509374 ref XP_001076719.1 PREDICTED: hypothetical protein	102	3e-20	G
gi 66802666 ref XP_635205.1 hypothetical protein DDBDRAFT_01...	102	3e-20	G
gi 66813268 ref XP_640813.1 SAP DNA-binding domain-containin...	102	3e-20	G
gi 5669894 gb AAD46501.1 AF148805_6 ORF73 [Human herpesvirus 8]	101	4e-20	

gi 11037008 gb AAG27458.1 AF305694_1	latent nuclear antigen [Hum	101	4e-20	
gi 109497810 ref XP_001058181.1 	PREDICTED: hypothetical protein	101	6e-20	G
gi 109487363 ref XP_001058747.1 	PREDICTED: hypothetical protein	100	8e-20	G
gi 109469884 ref XP_001063460.1 	PREDICTED: hypothetical protein	100	1e-19	G
gi 9886896 gb AAG01636.1 	Orf73 [Human herpesvirus 8]	100	1e-19	
gi 66810592 ref XP_639003.1 	hypothetical protein DDBDRAFT_01...	100	1e-19	G
gi 13936996 gb AAK50002.1 	ORF73 [Human herpesvirus 8]	99.8	2e-19	
gi 109464413 ref XP_001071056.1 	PREDICTED: hypothetical protein	99.4	2e-19	G
gi 94407897 ref XP_979552.1 	PREDICTED: hypothetical protein [Mu	99.4	2e-19	G
gi 2246532 gb AAB62657.1 	ORF 73 [Human herpesvirus 8]	99.4	2e-19	
gi 37725922 gb AAO38039.1 	reticulocyte binding-like protein 2b	99.0	3e-19	
gi 18846043 ref NP_572129.1 	ORF 73; extensive acidic domains...	99.0	3e-19	G
gi 66808553 ref XP_637999.1 	LIM domain-containing protein [D...	99.0	3e-19	G
gi 67477997 ref XP_654429.1 	Grainin 2 [Entamoeba histolytica...	98.6	4e-19	G
gi 28829643 gb AAO52159.1 	similar to C25A11.4b.p [Caenorhabd...	98.2	5e-19	
gi 66819811 ref XP_643564.1 	fimbrin-related RasGAP protein [...	98.2	5e-19	G
gi 111306569 gb AAI21747.1 	Unknown (protein for IMAGE:8158662)	97.8	6e-19	G
gi 92096287 gb AAI15075.1 	Unknown (protein for IMAGE:7448149) [97.8	6e-19	U G
gi 89286901 gb EAR84895.1 	hypothetical protein THERM_005845...	97.1	1e-18	
gi 38566922 emb CAE76225.1 	related to putative cytoplasmic s...	96.7	1e-18	
gi 85111555 ref XP_963992.1 	hypothetical protein [Neurospora...	96.7	1e-18	G
gi 66815949 ref XP_641991.1 	hypothetical protein DDBDRAFT_02...	96.3	2e-18	G
gi 109480597 ref XP_001053178.1 	PREDICTED: hypothetical protein	95.9	2e-18	G
gi 73981602 ref XP_540325.2 	PREDICTED: similar to Trichohyalin	95.9	2e-18	G
gi 66806319 ref XP_636882.1 	hypothetical protein DDBDRAFT_01...	95.9	2e-18	G
gi 82594248 ref XP_725343.1 	hypothetical protein PY04960 [Pl...	95.1	4e-18	G
gi 113420216 ref XP_001130141.1 	PREDICTED: hypothetical protein	94.4	7e-18	G
gi 56409774 emb CAF25315.1 	NBP2b protein [Plasmodium falciparum	94.4	7e-18	
gi 23508608 ref NP_701277.1 	hypothetical protein PF11_0418 [...	94.4	7e-18	E G
gi 66816387 ref XP_642203.1 	hypothetical protein DDB_0214889...	94.4	7e-18	G
gi 7549210 gb AAF63787.1 AF142406_1	200 kDa antigen p200 [Babesi	94.0	9e-18	
gi 73958144 ref XP_546992.2 	PREDICTED: similar to Zinc finge...	94.0	9e-18	G
gi 24580684 ref NP_608540.1 	CG2839-PA [Drosophila melanogast...	94.0	9e-18	U G
gi 67466733 ref XP_649508.1 	conserved hypothetical protein [...	94.0	9e-18	G
gi 94386777 ref XP_928149.2 	PREDICTED: hypothetical protein [Mu	93.6	1e-17	G
gi 23619293 ref NP_705255.1 	reticulocyte binding protein 2 h...	93.2	2e-17	E G
gi 13345187 gb AAK19244.1 AF312916_1	reticulocyte binding pro...	93.2	2e-17	
gi 437639 gb AAA72295.1 	[Plasmodium falciparum 3' end.], gene p	93.2	2e-17	
gi 23613070 ref NP_703392.1 	hypothetical protein [Plasmodium...	92.8	2e-17	E G
gi 66804281 ref XP_635920.1 	hypothetical protein DDBDRAFT_01...	92.4	3e-17	G
gi 109500521 ref XP_001075353.1 	PREDICTED: hypothetical protein	92.0	4e-17	G
gi 61353791 gb AAX44045.1 	clock [Macrobrachium rosenbergii]	92.0	4e-17	
gi 71548239 ref ZP_00668622.1 	similar to Chromosome segregat...	92.0	4e-17	
gi 66813088 ref XP_640723.1 	hypothetical protein DDBDRAFT_02...	91.7	5e-17	G
gi 109461086 ref XP_001068158.1 	PREDICTED: hypothetical protein	91.3	6e-17	G
gi 11493973 gb AAG35726.1 AF208229_1	lipase precursor GehM [Stap	91.3	6e-17	
gi 85104285 ref XP_961717.1 	hypothetical protein [Neurospora...	90.9	8e-17	G
gi 109493310 ref XP_001067694.1 	PREDICTED: similar to 60S ri...	90.5	1e-16	G
gi 109490763 ref XP_001075128.1 	PREDICTED: hypothetical protein	90.5	1e-16	G
gi 109501038 ref XP_001057439.1 	PREDICTED: hypothetical protein	89.7	2e-16	G
gi 109472820 ref XP_001076490.1 	PREDICTED: hypothetical protein	89.7	2e-16	G
gi 94396405 ref XP_984315.1 	PREDICTED: hypothetical protein [Mu	89.7	2e-16	G
gi 467292 gb AAA17387.1 	glutamine-asparagine rich protein	89.7	2e-16	

Alignments

Get selected sequences

Select all

Deselect all

> gi|510186|emb|CAA82974.1| liver stage antigen-1 [Plasmodium falciparum]
Length=318

Score = 441 bits (1135), Expect = 2e-122

Identities = 318/318 (100%), Positives = 318/318 (100%), Gaps = 0/318 (0%)

Frame = +1

Query	1	MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKsnlrsqssnsrnrineenheKKHV	180
		MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKSNLRSGSSNSRNRINEENHEKKHV	
Sbjct	1	MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKSNLRSGSSNSRNRINEENHEKKHV	60
Query	181	LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflkenklnke	360
		LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflKENKLNKE	
Sbjct	61	LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflKENKLNKE	120
Query	361	gkliehiinddddckkyikGQDENRQEDleekaakeklQGQQSDSEQERRAKEKLQEQQS	540
		GKLIEHIINDDDDCKKYIKGQDENRQEDLEEKAAKEKLQGQQSDSEQERRAKEKLQEQQS	
Sbjct	121	GKLIEHIINDDDDCKKYIKGQDENRQEDLEEKAAKEKLQGQQSDSEQERRAKEKLQEQQS	180
Query	541	DLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	720
		DLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	
Sbjct	181	DLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	240
Query	721	EKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSD	900
		EKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSD	
Sbjct	241	EKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSD	300
Query	901	LEQERRAKERLQEQQSDL	954
		LEQERRAKERLQEQQSDL	
Sbjct	301	LEQERRAKERLQEQQSDL	318

> gi|9916|emb|CAA39663.1| liver stage antigen [Plasmodium falciparum]
Length=1909

Score = 426 bits (1096), Expect = 6e-118

Identities = 309/318 (97%), Positives = 311/318 (97%), Gaps = 0/318 (0%)

Frame = +1

Query	1	MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKsnlrsqssnsrnrineenheKKHV	180
		MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKSNLRSGSSNSRNRINEE HEKKHV	
Sbjct	1	MKHILYISFYFILVNLLIFHINGKIIKNSEKDEIIKSNLRSGSSNSRNRINEEKHEKKHV	60
Query	181	LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflkenklnke	360
		LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflKENKLNKE	
Sbjct	61	LSHNSYEKTknnennkffdkdkeLTMSNVKNVSQTNFKSLLRNLGVSENIflKENKLNKE	120
Query	361	gkliehiinddddckkyikGQDENRQEDleekaakeklQGQQSDSEQERRAKEKLQEQQS	540
		GKLIEHIINDDDDCKKYIKGQDENRQEDLEEKAAKE LQGQQSD EQER AKEKLQEQQS	
Sbjct	121	GKLIEHIINDDDDCKKYIKGQDENRQEDLEEKAAKETLQGQQSDLEQERLAKEKLQEQQS	180
Query	541	DLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	720
		D EQERLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	
Sbjct	181	DSEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAK	240
Query	721	EKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSD	900
		EKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQ+RLAKEKLQEQQSD	
Sbjct	241	EKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSD	300

Query 901 LEQERRAKERLQEQQSDL 954
LEQERRAKE+LQEQQSDL
Sbjct 301 LEQERRAKEKLQEQQSDL 318

Score = 287 bits (735), Expect = 4e-76
Identities = 153/160 (95%), Positives = 156/160 (97%), Gaps = 0/160 (0%)
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ
Sbjct 805 QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 864

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
+RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ
Sbjct 865 DRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 924

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
EQQ DLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL
Sbjct 925 EQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 964

Score = 287 bits (734), Expect = 6e-76
Identities = 153/160 (95%), Positives = 156/160 (97%), Gaps = 0/160 (0%)
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
Q QQSD EQERRAKEKLQEQQSDLEQ+RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ
Sbjct 737 QEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 796

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
+RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQ
Sbjct 797 DRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQ 856

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
EQQSDLEQDRLAKEKLQEQQSDLEQERRAKE+LQEQQSDL
Sbjct 857 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 896

Score = 284 bits (726), Expect = 5e-75
Identities = 152/160 (95%), Positives = 155/160 (96%), Gaps = 0/160 (0%)
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
Q QQSD EQ+R AKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ
Sbjct 380 QEQQSDLEQDRLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 439

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ
Sbjct 440 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 499

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
EQQSDLEQ+RLAKEKLQEQQSD EQER AKE+LQEQQSDL
Sbjct 500 EQQSDLEQERLAKEKLQEQQSDSEQERLAKEKLQEQQSDL 539

Score = 283 bits (725), Expect = 6e-75
Identities = 153/160 (95%), Positives = 154/160 (96%), Gaps = 0/160 (0%)
Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ
Sbjct 261 QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 320

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834

Sbjct 321 ERLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQ QQSDLEQERLAKEKLQ 380
 ERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQGGQSDLEQERLAKEKLQ

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQSDLEQDRLAKEKLQEQQSDLEQER AKE+LQEQQSDL

Sbjct 381 EQQSDLEQDRLAKEKLQEQQSDLEQERLAKEKLQEQQSDL 420

Score = 283 bits (724), Expect = 8e-75
 Identities = 151/160 (94%), Positives = 155/160 (96%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
 Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ

Sbjct 703 QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 762

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
 +RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQER AKEKLQ

Sbjct 763 DRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQ 822

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQSDLEQ+RLAKEKLQEQQSDLEQERRAKE+LQEQQSDL

Sbjct 823 EQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 862

Score = 283 bits (724), Expect = 8e-75
 Identities = 151/160 (94%), Positives = 154/160 (96%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
 Q QQSD EQERRAKEKLQEQQSDLEQ+RLAKEKLQEQQ DLEQERRAKEKLQEQQSDLEQ

Sbjct 1366 QEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 1425

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
 ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ

Sbjct 1426 ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 1485

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQ DLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL

Sbjct 1486 EQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1525

Score = 283 bits (723), Expect = 1e-74
 Identities = 152/160 (95%), Positives = 154/160 (96%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
 Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQ

Sbjct 1196 QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ 1255

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
 ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ

Sbjct 1256 ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 1315

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQSDLEQ+RLAKEKLQEQQSDLEQERRAKE+LQEQQSDL

Sbjct 1316 EQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1355

Score = 283 bits (723), Expect = 1e-74
 Identities = 152/160 (95%), Positives = 154/160 (96%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
 Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ

Sbjct	1213	QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1272
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERLAKEKLQ	834
Sbjct	1273	ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQ	1332
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQ+R AKEKLQEQQSDLEQER AKE+LQEQQSDL	
Sbjct	1333	EQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDL 1372	

Score = 282 bits (722), Expect = 1e-74
Identities = 152/160 (95%), Positives = 154/160 (96%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
Sbjct	227	QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	286
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERLAKEKLQ	834
Sbjct	287	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQ	346
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQ+RLAKEKLQ QQSDLEQER AKE+LQEQQSDL	
Sbjct	347	EQQSDLEQERLAKEKLQGQQSDLEQERLAKEKLQEQQSDL 386	

Score = 282 bits (722), Expect = 1e-74
Identities = 152/160 (95%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQ	654
Sbjct	1264	QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ	1323
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQ	834
Sbjct	1324	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQ	1383
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQDRLAKEKLQEQQ DLEQERRAKE+LQEQQSDL	
Sbjct	1384	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1423	

Score = 282 bits (722), Expect = 1e-74
Identities = 151/160 (94%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
Sbjct	1417	QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1476
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ERLAKEKLQEQQ DLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLA EKLQ	834
Sbjct	1477	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLANEKLQ	1536
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQ DLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL	
Sbjct	1537	EQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1576	

Score = 281 bits (718), Expect = 4e-74
Identities = 151/160 (94%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	669	QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	728
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQER AKEKLQ	
Sbjct	729	ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQ	788
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL	954
		EQQSDLEQDRLAKEKLQEQQSDLEQERRAKE+LQEQQSDL	
Sbjct	789	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDL	828

Score = 280 bits (717), Expect = 5e-74
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	1332	QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1391
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		+RLAKEKLQEQQ DLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQ	
Sbjct	1392	DRLAKEKLQEQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ	1451
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL	954
		EQQSDLEQ+R AKEKLQEQQSDLEQER AKE+LQEQQ DL	
Sbjct	1452	EQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQRDL	1491

Score = 280 bits (716), Expect = 7e-74
Identities = 151/160 (94%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	414	QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	473
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSD EQERLAKEKLQ	
Sbjct	474	ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDSEQERLAKEKLQ	533
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL	954
		EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSDL	
Sbjct	534	EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDL	573

Score = 280 bits (715), Expect = 9e-74
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQERRAKEKLQEQQSDLEQ+RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	839	QEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	898
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ER AKEKLQEQQSDLEQER AKEKLQEQQ DLEQERRAKEKLQEQQSDLEQER AKEKLQ	
Sbjct	899	ERRAKEKLQEQQSDLEQERLAKEKLQEQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQ	958
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL	954
		EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSDL	
Sbjct	959	EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDL	998

Score = 280 bits (715), Expect = 9e-74
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	1247	QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1306
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ERLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	
Sbjct	1307	ERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	1366
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954	
		EQQSDLEQ+R AKEKLQEQQSDLEQ+R AKE+LQEQQ DL	
Sbjct	1367	EQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQRDL 1406	

Score = 280 bits (715), Expect = 9e-74
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQ	
Sbjct	1281	QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ	1340
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+RLAKEKLQ	
Sbjct	1341	ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQ	1400
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954	
		EQQ DLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL	
Sbjct	1401	EQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1440	

Score = 280 bits (715), Expect = 9e-74
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQER AKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	1298	QEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1357
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+R AKEKLQEQQ DLEQER AKEKLQ	
Sbjct	1358	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQRDLEQERRAKEKLQ	1417
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954	
		EQQSDLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL	
Sbjct	1418	EQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1457	

Score = 279 bits (714), Expect = 1e-73
Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
		Q QQSD EQ+R AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	
Sbjct	856	QEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	915
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	834
		ERLAKEKLQEQQ DLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	
Sbjct	916	ERLAKEKLQEQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ	975
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954	
		EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQ QQSDL	

Sbjct 976 EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQGGQSDL 1015

Score = 278 bits (712), Expect = 2e-73

Identities = 150/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)

Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654

Q QQSD EQER AKEKLQEQQSDLEQERLAKEKLQ QQSDLEQER AKEKLQEQQSDLEQ

Sbjct 329 QEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQGGQSDLEQERLAKEKLQEQQSDLEQ 388

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834

+RLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ

Sbjct 389 DRLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 448

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954

EQQSDLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL

Sbjct 449 EQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 488

Score = 278 bits (712), Expect = 2e-73

Identities = 149/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)

Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654

Q QQSD EQERRAKEKLQEQQSDLEQ+RLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ

Sbjct 771 QEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 830

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834

ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQER AKEKLQ

Sbjct 831 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQ 890

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954

EQQSDLEQ+R AKEKLQEQQSDLEQER AKE+LQEQQ DL

Sbjct 891 EQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQRDL 930

Score = 278 bits (711), Expect = 3e-73

Identities = 149/160 (93%), Positives = 153/160 (95%), Gaps = 0/160 (0%)

Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654

Q QQSD EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ

Sbjct 686 QEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 745

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834

ER AKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ+RLAKEKLQ

Sbjct 746 ERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQ 805

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954

EQQSDLEQ+R AKEKLQEQQSDLEQER AKE+LQEQQSDL

Sbjct 806 EQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDL 845

Score = 278 bits (710), Expect = 3e-73

Identities = 149/159 (93%), Positives = 152/159 (95%), Gaps = 0/159 (0%)

Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654

QGQQSD EQER AKEKLQEQQSDLEQ+RLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQ

Sbjct 363 QGQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ 422

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834

ER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQ

Sbjct 423 ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ 482

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSD 951
 EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSD
 Sbjct 483 EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSD 521

Score = 278 bits (710), Expect = 3e-73
 Identities = 148/160 (92%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
 QGQQSD EQER AKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLE+
 Sbjct 1128 QGQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLER 1187

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
 + +KE LQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ
 Sbjct 1188 TKASKETLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 1247

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQSDLEQ+R AKEKLQEQQSDLEQERRAKE+LQEQQSDL
 Sbjct 1248 EQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1287

Score = 278 bits (710), Expect = 3e-73
 Identities = 150/160 (93%), Positives = 152/160 (95%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
 Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ
 Sbjct 1230 QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 1289

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
 ER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQ
 Sbjct 1290 ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQ 1349

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQSDLEQ+RLAKEKLQEQQSDLEQERRAKE+LQEQQSDL
 Sbjct 1350 EQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 1389

Score = 277 bits (709), Expect = 5e-73
 Identities = 150/160 (93%), Positives = 152/160 (95%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
 Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ
 Sbjct 431 QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 490

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
 ERLAKEKLQEQQSDLEQER AKEKLQEQQSD EQER AKEKLQEQQSDLEQERLAKEKLQ
 Sbjct 491 ERLAKEKLQEQQSDLEQERLAKEKLQEQQSDSEQERLAKEKLQEQQSDLEQERLAKEKLQ 550

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSDL
 Sbjct 551 EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDL 590

Score = 277 bits (708), Expect = 6e-73
 Identities = 148/160 (92%), Positives = 153/160 (95%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
 Q QQSD E+ + +KE LQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ
 Sbjct 1179 QEQQSDLERTKASKETLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 1238

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQ
 Sbjct 1239 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ 1298

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQSDLEQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSDL
 Sbjct 1299 EQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDL 1338

Score = 276 bits (707), Expect = 8e-73
 Identities = 154/177 (87%), Positives = 155/177 (87%), Gaps = 17/177 (9%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEK-----LQEQQSDLEQ 603
 QGQQSD EQER AKEKLQEQQSDLEQERLAKEK LQEQQSDLEQ
 Sbjct 618 QGQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLERTKASKETLQEQQSDLEQ 677

Query 604 ERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ 783
 ER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ
 Sbjct 678 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ 737

Query 784 EQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQSDLEQER AKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKE+LQEQQSDL
 Sbjct 738 EQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 794

Score = 276 bits (705), Expect = 1e-72
 Identities = 149/160 (93%), Positives = 152/160 (95%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
 Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQ
 Sbjct 278 QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ 337

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
 ERLAKEKLQEQQSDLEQER AKEKLQ QQSDLEQER AKEKLQEQQSDLEQ+RLAKEKLQ
 Sbjct 338 ERLAKEKLQEQQSDLEQERLAKEKLQGGQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQ 397

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQSDLEQ+RLAKEKLQEQQSDLEQERRAKE+LQEQQSDL
 Sbjct 398 EQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 437

Score = 276 bits (705), Expect = 1e-72
 Identities = 149/160 (93%), Positives = 152/160 (95%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654
 Q QQSD EQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQER AKEKLQEQQSDLEQ
 Sbjct 295 QEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ 354

Query 655 ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ 834
 ERLAKEKLQ QQSDLEQER AKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQERLAKEKLQ
 Sbjct 355 ERLAKEKLQGGQQSDLEQERLAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERLAKEKLQ 414

Query 835 EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954
 EQQSDLEQ+R AKEKLQEQQSDLEQER AKE+LQEQQSDL
 Sbjct 415 EQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDL 454

Score = 276 bits (705), Expect = 1e-72
 Identities = 149/160 (93%), Positives = 152/160 (95%), Gaps = 0/160 (0%)
 Frame = +1

Query 475 QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ 654

Sbjct	312	Q QQSD EQER AKEKLQEQQSDLEQERLAKEKLQEQQSDLEQER AKEKLQ QQSDLEQ QEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQGGQSDLEQ	371
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ERLAKEKLQEQQSDLEQ+R AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQ	834
Sbjct	372	ERLAKEKLQEQQSDLEQDRLAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQ	431
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQ+RLAKEKLQEQQSDLEQERRAKE+LQEQQSDL	
Sbjct	432	EQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDL 471	

Score = 275 bits (704), Expect = 2e-72
Identities = 148/160 (92%), Positives = 151/160 (94%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQ+R AKEKLQEQQ DLEQ	654
Sbjct	1349	QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQRDLEQ	1408
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQ	834
Sbjct	1409	ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQ	1468
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQ+RLAKEKLQEQQ DLEQERRAKE+LQEQQSDL	
Sbjct	1469	EQQSDLEQERLAKEKLQEQQRDLEQERRAKEKLQEQQSDL 1508	

Score = 275 bits (704), Expect = 2e-72
Identities = 148/160 (92%), Positives = 150/160 (93%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQ D EQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	654
Sbjct	1400	QEQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ	1459
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ER AKEKLQEQQSDLEQER AKEKLQEQQ DLEQERRAKEKLQEQQSDLEQER AKEKLQ	834
Sbjct	1460	ERRAKEKLQEQQSDLEQERLAKEKLQEQQRDLEQERRAKEKLQEQQSDLEQERRAKEKLQ	1519
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSDLEQ+RLA EKLQEQQ DLEQERRAKE+LQEQQSDL	
Sbjct	1520	EQQSDLEQERLANEKLQEQQRDLEQERRAKEKLQEQQSDL 1559	

Score = 275 bits (703), Expect = 2e-72
Identities = 149/160 (93%), Positives = 151/160 (94%), Gaps = 0/160 (0%)
Frame = +1

Query	475	QGQQSDSEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQ Q QQSD EQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQER AKEKLQEQQSDLEQ	654
Sbjct	397	QEQQSDLEQERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQ	456
Query	655	ERLAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQ ER AKEKLQEQQSDLEQERRAKEKLQEQQSDLEQER AKEKLQEQQSDLEQERLAKEKLQ	834
Sbjct	457	ERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQSDLEQERLAKEKLQ	516
Query	835	EQQSDLEQDRLAKEKLQEQQSDLEQERRAKERLQEQQSDL 954 EQQSD EQ+RLAKEKLQEQQSDLEQER AKE+LQEQQSDL	
Sbjct	517	EQQSDSEQERLAKEKLQEQQSDLEQERLAKEKLQEQQSDL 556	

Score = 275 bits (703), Expect = 2e-72
Identities = 149/160 (93%), Positives = 151/160 (94%), Gaps = 0/160 (0%)